Effect of Polydextrose Supplementation on Gut Microbiota After Gastrectomy in Rats

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BACKGROUND: The gastrectomy consists in a surgical treatment for gastric cancer, a chronic multifactorial disease that causes numerous deaths worldwide. As a consequence of surgery, mineral absorption could be decreased. Otherwise different studies suggested that supplementation with polydextrose is capable of modulate the gut microbiota showing an important role in assisting in the absorption process after gastrectomy. **OBJECTIVE:** This study aims to describe and compare the variability of the bacterial community in relation to polydextrose supplementation during 21 days on gut microbiota after gastrectomy in rats. MATERIAL AND **METHODS:** Fecal samples collected from 5 different treatments: G1 G2 (Gastrectomized rats fed with AIN-93M plus 7.5% polydextrose). (Gastrectomized rats fed with AIN-93M without polydextrose), G3 (Sham-operated rats fed with AIN-93M plus 7.5% polydextrose), G4 (Sham-operated rats fed with AIN-93M without polydextrose) and G5 (Non-operated rats fed with AIN-93M without polydextrose) was used for access the relationship among polydextrose supplementation, gastrectomy and gut microbiota. By using rDNA genes barcode analysis, a total of the 21 million reads were performed to assess the bacterial diversity. **DISCUSSION AND RESULTS**: Comparative analysis revealed a distinct distribution of bacterial diversity before and after polydextrose supplementation. According to the OTU richness estimated by Shannon index, there was a greater diversity of bacterial communities after polydextrose supplementation when compared to control group. The relative abundances of Clostridium and Streptococcus showed decreased in relation of polydextrose supplementation. In contrast, Bacteroides, Lactococcus and Prevotella seem to be enriched after gastrectomy. CONCLUSIONS: These results may help answer questions about how the supplementation with polydextrose can influenced the gut microbiota after gastrectomy. In summary, this is the first culture independent analysis of the gut bacterial community diversity from gastrectomy in rats.

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